



## **Comparative transcriptomics of caste development across multiple origins of eusociality**

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Reproductive division of labor via caste has evolved many times in insects and is responsible for the immense ecological success of social insects. It has been hypothesized that there exists a core set of genes associated with each origin of reproductive caste, but studies have largely failed to identify such a core set. Here, we present the most comprehensive transcriptomic comparison to date of caste development across multiple origins of eusociality. We perform RNA-sequencing across development of queens and workers in the honey bee *Apis mellifera* and ant *Monomorium pharaonis*. We seek to identify a core set of genes commonly associated with caste development in each species, which we term a caste toolkit. We test if this caste toolkit, and a related social toolkit derived from comparisons between nurses and foragers, is rooted in common core developmental processes. This study will provide a foundation with which to test whether convergent molecular mechanisms underlie key innovations associated with the repeated evolution of eusociality.